

030/0190

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/044,303

DATE: 04/18/2002 PS  
 TIME: 11:06:15

Input Set : A:\Vectors1.app  
 Output Set: N:\CRF3\04182002\J044303.raw

3 <110> APPLICANT: Max-Planck-Gesellschaft e.V.  
 5 <120> TITLE OF INVENTION: Protein expression and structure solution using  
 6 specific fusion vectors  
 8 <130> FILE REFERENCE: ST010209-EPA  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/044,303  
 C--> 11 <141> CURRENT FILING DATE: 2002-01-11  
 13 <160> NUMBER OF SEQ ID NOS: 3  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 765  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial myosin  
 24 sequence of Dictyostelium; Component (1) of the  
 25 recombinant protein M761-2R R238E  
 27 <400> SEQUENCE: 1  
 28 Met Asp Gly Thr Glu Asp Pro Ile His Asp Arg Thr Ser Asp Tyr His  
 29 1 5 10 15  
 31 Lys Tyr Leu Lys Val Lys Gln Gly Asp Ser Asp Leu Phe Lys Leu Thr  
 32 20 25 30  
 34 Val Ser Asp Lys Arg Tyr Ile Trp Tyr Asn Pro Asp Pro Lys Glu Arg  
 35 35 40 45  
 37 Asp Ser Tyr Glu Cys Gly Glu Ile Val Ser Glu Thr Ser Asp Ser Phe  
 38 50 55 60  
 40 Thr Phe Lys Thr Val Asp Gly Gln Asp Arg Gln Val Lys Lys Asp Asp  
 41 65 70 75 80  
 43 Ala Asn Gln Arg Asn Pro Ile Lys Phe Asp Gly Val Glu Asp Met Ser  
 44 85 90 95  
 46 Glu Leu Ser Tyr Leu Asn Glu Pro Ala Val Phe His Asn Leu Arg Val  
 47 100 105 110  
 49 Arg Tyr Asn Gln Asp Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Leu Val  
 50 115 120 125  
 52 Ala Val Asn Pro Phe Lys Arg Ile Pro Ile Tyr Thr Gln Glu Met Val  
 53 130 135 140  
 55 Asp Ile Phe Lys Gly Arg Arg Asn Glu Val Ala Pro His Ile Phe  
 56 145 150 155 160  
 58 Ala Ile Ser Asp Val Ala Tyr Arg Ser Met Leu Asp Asp Arg Gln Asn  
 59 165 170 175  
 61 Gln Ser Leu Leu Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn  
 62 180 185 190  
 64 Thr Lys Lys Val Ile Gln Tyr Leu Ala Ser Val Ala Gly Arg Asn Gln  
 65 195 200 205

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67 Ala Asn Gly Ser Gly Val Leu Glu Gln Gln Ile Leu Gln Ala Asn Pro  
 68 210 215 220  
 70 Ile Leu Glu Ala Phe Gly Asn Ala Lys Thr Thr Arg Asn Asn Asn Ser  
 71 225 230 235 240  
 73 Ser Arg Phe Gly Lys Phe Ile Glu Ile Gln Phe Asn Ser Ala Gly Phe  
 74 245 250 255  
 76 Ile Ser Gly Ala Ser Ile Gln Ser Tyr Leu Leu Glu Lys Ser Arg Val  
 77 260 265 270  
 79 Val Phe Gln Ser Glu Thr Glu Arg Asn Tyr His Ile Phe Tyr Gln Leu  
 80 275 280 285  
 82 Leu Ala Gly Ala Thr Ala Glu Glu Lys Lys Ala Leu His Leu Ala Gly  
 83 290 295 300  
 85 Pro Glu Ser Phe Asn Tyr Leu Asn Gln Ser Gly Cys Val Asp Ile Lys  
 86 305 310 315 320  
 88 Gly Val Ser Asp Ser Glu Glu Phe Lys Ile Thr Arg Gln Ala Met Asp  
 89 325 330 335  
 91 Ile Val Gly Phe Ser Gln Glu Glu Gln Met Ser Ile Phe Lys Ile Ile  
 92 340 345 350  
 94 Ala Gly Ile Leu His Leu Gly Asn Ile Lys Phe Glu Lys Gly Ala Gly  
 95 355 360 365  
 97 Glu Gly Ala Val Leu Lys Asp Lys Thr Ala Leu Asn Ala Ala Ser Thr  
 98 370 375 380  
 100 Val Phe Gly Val Asn Pro Ser Val Leu Glu Lys Ala Leu Met Glu Pro  
 101 385 390 395 400  
 103 Arg Ile Leu Ala Gly Arg Asp Leu Val Ala Gln His Leu Asn Val Glu  
 104 405 410 415  
 106 Lys Ser Ser Ser Arg Asp Ala Leu Val Lys Ala Leu Tyr Gly Arg  
 107 420 425 430  
 109 Leu Phe Leu Trp Leu Val Lys Ile Asn Asn Val Leu Cys Gln Glu  
 110 435 440 445  
 112 Arg Lys Ala Tyr Phe Ile Gly Val Leu Asp Ile Ser Gly Phe Glu Ile  
 113 450 455 460  
 115 Phe Lys Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn Glu  
 116 465 470 475 480  
 118 Lys Leu Gln Gln Phe Phe Asn His His Met Phe Lys Leu Glu Gln Glu  
 119 485 490 495  
 121 Glu Tyr Leu Lys Glu Lys Ile Asn Trp Thr Phe Ile Asp Phe Gly Leu  
 122 500 505 510  
 124 Asp Ser Gln Ala Thr Ile Asp Leu Ile Asp Gly Arg Gln Pro Pro Gly  
 125 515 520 525  
 127 Ile Leu Ala Leu Leu Asp Glu Gln Ser Val Phe Pro Asn Ala Thr Asp  
 128 530 535 540  
 130 Asn Thr Leu Ile Thr Lys Leu His Ser His Phe Ser Lys Lys Asn Ala  
 131 545 550 555 560  
 133 Lys Tyr Glu Glu Pro Arg Phe Ser Lys Thr Glu Phe Gly Val Thr His  
 134 565 570 575  
 136 Tyr Ala Gly Gln Val Met Tyr Glu Ile Gln Asp Trp Leu Glu Lys Asn  
 137 580 585 590  
 139 Lys Asp Pro Leu Gln Gln Asp Leu Glu Leu Cys Phe Lys Asp Ser Ser

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Input Set : A:\Vectors1.app  
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140	595	600	605
142	Asp Asn Val Val Thr Lys Leu Phe Asn Asp Pro Asn Ile Ala Ser Arg		
143	610	615	620
145	Ala Lys Lys Gly Ala Asn Phe Ile Thr Val Ala Ala Gln Tyr Lys Glu		
146	625	630	635
148	Gln Leu Ala Ser Leu Met Ala Thr Leu Glu Thr Thr Asn Pro His Phe		
149	645	650	655
151	Val Arg Cys Ile Ile Pro Asn Asn Lys Gln Leu Pro Ala Lys Leu Glu		
152	660	665	670
154	Asp Lys Val Val Leu Asp Gln Leu Arg Cys Asn Gly Val Leu Glu Gly		
155	675	680	685
157	Ile Arg Ile Thr Arg Lys Gly Phe Pro Asn Arg Ile Ile Tyr Ala Asp		
158	690	695	700
160	Phe Val Lys Arg Tyr Tyr Leu Leu Ala Pro Asn Val Pro Arg Asp Ala		
161	705	710	715
163	Glu Asp Ser Gln Lys Ala Thr Asp Ala Val Leu Lys His Leu Asn Ile		
164	725	730	735
166	Asp Pro Glu Gln Tyr Arg Phe Gly Ile Thr Lys Ile Phe Phe Arg Ala		
167	740	745	750
169	Gly Gln Leu Ala Arg Ile Glu Glu Ala Arg Glu Gln Arg		
170	755	760	765
173	<210> SEQ ID NO: 2		
174	<211> LENGTH: 1016		
175	<212> TYPE: PRT		
176	<213> ORGANISM: Artificial Sequence		
178	<220> FEATURE:		
179	<223> OTHER INFORMATION: Description of Artificial Sequence: Whole sequence		
180	of recombinant protein M761-2R R238 E		
182	<220> FEATURE:		
183	<223> OTHER INFORMATION: The protein comprises as component (1) the aa		
184	sequence of myosin II motor domain of		
185	Dictyostelium, a three aa linker region and the		
186	a-actinin aa sequence		
188	<400> SEQUENCE: 2		
189	Met Asp Gly Thr Glu Asp Pro Ile His Asp Arg Thr Ser Asp Tyr His		
190	1	5	10
192	Lys Tyr Leu Lys Val Lys Gln Gly Asp Ser Asp Leu Phe Lys Leu Thr		
193	20	25	30
195	Val Ser Asp Lys Arg Tyr Ile Trp Tyr Asn Pro Asp Pro Lys Glu Arg		
196	35	40	45
198	Asp Ser Tyr Glu Cys Gly Glu Ile Val Ser Glu Thr Ser Asp Ser Phe		
199	50	55	60
201	Thr Phe Lys Thr Val Asp Gly Gln Asp Arg Gln Val Lys Lys Asp Asp		
202	65	70	75
204	Ala Asn Gln Arg Asn Pro Ile Lys Phe Asp Gly Val Glu Asp Met Ser		
205	85	90	95
207	Glu Leu Ser Tyr Leu Asn Glu Pro Ala Val Phe His Asn Leu Arg Val		
208	100	105	110
210	Arg Tyr Asn Gln Asp Leu Ile Tyr Thr Ser Gly Leu Phe Leu Val		

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Input Set : A:\Vectors1.app  
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211	115	120	125
213	Ala Val Asn Pro Phe Lys Arg Ile Pro Ile Tyr Thr Gln Glu Met Val		
214	130	135	140
216	Asp Ile Phe Lys Gly Arg Arg Arg Asn Glu Val Ala Pro His Ile Phe		
217	145	150	155
219	Ala Ile Ser Asp Val Ala Tyr Arg Ser Met Leu Asp Asp Arg Gln Asn		
220	165	170	175
222	Gln Ser Leu Leu Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn		
223	180	185	190
225	Thr Lys Lys Val Ile Gln Tyr Leu Ala Ser Val Ala Gly Arg Asn Gln		
226	195	200	205
228	Ala Asn Gly Ser Gly Val Leu Glu Gln Gln Ile Leu Gln Ala Asn Pro		
229	210	215	220
231	Ile Leu Glu Ala Phe Gly Asn Ala Lys Thr Thr Arg Asn Asn Asn Ser		
232	225	230	235
234	Ser Arg Phe Gly Lys Phe Ile Glu Ile Gln Phe Asn Ser Ala Gly Phe		
235	245	250	255
237	Ile Ser Gly Ala Ser Ile Gln Ser Tyr Leu Leu Glu Lys Ser Arg Val		
238	260	265	270
240	Val Phe Gln Ser Glu Thr Glu Arg Asn Tyr His Ile Phe Tyr Gln Leu		
241	275	280	285
243	Leu Ala Gly Ala Thr Ala Glu Glu Lys Lys Ala Leu His Leu Ala Gly		
244	290	295	300
246	Pro Glu Ser Phe Asn Tyr Leu Asn Gln Ser Gly Cys Val Asp Ile Lys		
247	305	310	315
249	Gly Val Ser Asp Ser Glu Glu Phe Lys Ile Thr Arg Gln Ala Met Asp		
250	325	330	335
252	Ile Val Gly Phe Ser Gln Glu Glu Gln Met Ser Ile Phe Lys Ile Ile		
253	340	345	350
255	Ala Gly Ile Leu His Leu Gly Asn Ile Lys Phe Glu Lys Gly Ala Gly		
256	355	360	365
258	Glu Gly Ala Val Leu Lys Asp Lys Thr Ala Leu Asn Ala Ala Ser Thr		
259	370	375	380
261	Val Phe Gly Val Asn Pro Ser Val Leu Glu Lys Ala Leu Met Glu Pro		
262	385	390	395
264	Arg Ile Leu Ala Gly Arg Asp Leu Val Ala Gln His Leu Asn Val Glu		
265	405	410	415
267	Lys Ser Ser Ser Arg Asp Ala Leu Val Lys Ala Leu Tyr Gly Arg		
268	420	425	430
270	Leu Phe Leu Trp Leu Val Lys Lys Ile Asn Asn Val Leu Cys Gln Glu		
271	435	440	445
273	Arg Lys Ala Tyr Phe Ile Gly Val Leu Asp Ile Ser Gly Phe Glu Ile		
274	450	455	460
276	Phe Lys Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn Glu		
277	465	470	475
279	Lys Leu Gln Gln Phe Phe Asn His His Met Phe Lys Leu Glu Gln Glu		
280	485	490	495
282	Glu Tyr Leu Lys Glu Lys Ile Asn Trp Thr Phe Ile Asp Phe Gly Leu		
283	500	505	510

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Input Set : A:\Vectors1.app  
Output Set: N:\CRF3\04182002\J044303.raw

```

285 Asp Ser Gln Ala Thr Ile Asp Leu Ile Asp Gly Arg Gln Pro Pro Gly
286      515           520           525
288 Ile Leu Ala Leu Leu Asp Glu Gln Ser Val Phe Pro Asn Ala Thr Asp
289      530           535           540
291 Asn Thr Leu Ile Thr Lys Leu His Ser His Phe Ser Lys Lys Asn Ala
292 545           550           555           560
294 Lys Tyr Glu Glu Pro Arg Phe Ser Lys Thr Glu Phe Gly Val Thr His
295           565           570           575
297 Tyr Ala Gly Gln Val Met Tyr Glu Ile Gln Asp Trp Leu Glu Lys Asn
298           580           585           590
300 Lys Asp Pro Leu Gln Gln Asp Leu Glu Leu Cys Phe Lys Asp Ser Ser
301           595           600           605
303 Asp Asn Val Val Thr Lys Leu Phe Asn Asp Pro Asn Ile Ala Ser Arg
304           610           615           620
306 Ala Lys Lys Gly Ala Asn Phe Ile Thr Val Ala Ala Gln Tyr Lys Glu
307 625           630           635           640
309 Gln Leu Ala Ser Leu Met Ala Thr Leu Glu Thr Thr Asn Pro His Phe
310           645           650           655
312 Val Arg Cys Ile Ile Pro Asn Asn Lys Gln Leu Pro Ala Lys Leu Glu
313           660           665           670
315 Asp Lys Val Val Leu Asp Gln Leu Arg Cys Asn Gly Val Leu Glu Gly
316           675           680           685
318 Ile Arg Ile Thr Arg Lys Gly Phe Pro Asn Arg Ile Ile Tyr Ala Asp
319           690           695           700
321 Phe Val Lys Arg Tyr Tyr Leu Leu Ala Pro Asn Val Pro Arg Asp Ala
322 705           710           715           720
324 Glu Asp Ser Gln Lys Ala Thr Asp Ala Val Leu Lys His Leu Asn Ile
325           725           730           735
327 Asp Pro Glu Gln Tyr Arg Phe Gly Ile Thr Lys Ile Phe Phe Arg Ala
328           740           745           750
330 Gly Gln Leu Ala Arg Ile Glu Glu Ala Arg Glu Gln Arg Leu Gly Ser
331           755           760           765
333 Glu Gln Thr Lys Ser Asp Tyr Leu Lys Arg Ala Asn Glu Leu Val Gln
334           770           775           780
336 Trp Ile Asn Asp Lys Gln Ala Ser Leu Glu Ser Arg Asp Phe Gly Asp
337 785           790           795           800
339 Ser Ile Glu Ser Val Gln Ser Phe Met Asn Ala His Lys Glu Tyr Lys
340           805           810           815
342 Lys Thr Glu Lys Pro Pro Lys Gly Gln Glu Val Ser Glu Leu Glu Ala
343           820           825           830
345 Ile Tyr Asn Ser Leu Gln Thr Lys Leu Arg Leu Ile Lys Arg Glu Pro
346           835           840           845
348 Phe Val Ala Pro Ala Gly Leu Thr Pro Asn Glu Ile Asp Ser Thr Trp
349           850           855           860
351 Ser Ala Leu Glu Lys Ala Glu Gln Glu His Ala Glu Ala Leu Arg Ile
352 865           870           875           880
354 Glu Leu Lys Arg Gln Lys Lys Ile Ala Val Leu Leu Gln Lys Tyr Asn
355           885           890           895
357 Arg Ile Leu Lys Lys Leu Glu Asn Trp Ala Thr Thr Lys Ser Val Tyr

```

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/044,303

DATE: 04/18/2002

TIME: 11:06:16

Input Set : A:\Vectors1.app

Output Set: N:\CRF3\04182002\J044303.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:424 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3

L:424 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3

L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3